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# 2

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,401A

DATE: 01/09/2003

TIME: 07:48:08

Input Set : N:\Cr3\RULE60\09879401.raw.txt

Output Set: N:\CRF4\01092003\I879401A.raw

## SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: Lal, Preeti
6       Hillman, Jennifer
7       Corley, Neil
8       Shah, Purvi
10  (ii) TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS
12  (iii) NUMBER OF SEQUENCES: 6
14  (iv) CORRESPONDENCE ADDRESS:
15      (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16      (B) STREET: 3174 Porter Dr.
17      (C) CITY: Palo Alto
18      (D) STATE: CA
19      (E) COUNTRY: USA
20      (F) ZIP: 94304
22  (v) COMPUTER READABLE FORM:
23      (A) MEDIUM TYPE: Diskette
24      (B) COMPUTER: IBM Compatible
25      (C) OPERATING SYSTEM: DOS
26      (D) SOFTWARE: FastSEQ for Windows Version 2.0
28  (vi) CURRENT APPLICATION DATA:
C--> 29      (A) APPLICATION NUMBER: US/09/879,401A
C--> 30      (B) FILING DATE: 13-Jun-2001
31      (C) CLASSIFICATION:
33  (vii) PRIOR APPLICATION DATA:
34      (A) APPLICATION NUMBER: US/08/958,820
35      (B) FILING DATE: Filed Herewith
38  (viii) ATTORNEY/AGENT INFORMATION:
39      (A) NAME: Billings, Lucy J.
40      (B) REGISTRATION NUMBER: 36,749
41      (C) REFERENCE/DOCKET NUMBER: PF-0379 US
43  (ix) TELECOMMUNICATION INFORMATION:
44      (A) TELEPHONE: 650-855-0555
45      (B) TELEFAX: 650-845-4166
48 (2) INFORMATION FOR SEQ ID NO: 1:
50   (i) SEQUENCE CHARACTERISTICS:
51      (A) LENGTH: 214 amino acids
52      (B) TYPE: amino acid
53      (C) STRANDEDNESS: single
54      (D) TOPOLOGY: linear
56  (vii) IMMEDIATE SOURCE:
57      (A) LIBRARY: MUSCNOT07
58      (B) CLONE: 3014759

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62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 64 Met Glu Leu Ala Ala Gly Ser Phe Ser Glu Glu Gln Phe Trp Glu Ala  
 65 1 5 10 15  
 66 Cys Ala Glu Leu Gln Gln Pro Ala Leu Ala Gly Ala Asp Trp Gln Leu  
 67 20 25 30  
 68 Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys  
 69 35 40 45  
 70 Thr Gly Leu Tyr Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser  
 71 50 55 60  
 72 Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln  
 73 65 70 75 80  
 74 Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu  
 75 85 90 95  
 76 Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg  
 77 100 105 110  
 78 Asp Tyr Val Tyr Leu Arg Gln Arg Arg Asp Leu Asp Met Glu Gly Arg  
 79 115 120 125  
 80 Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly  
 81 130 135 140  
 82 Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala  
 83 145 150 155 160  
 84 Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe  
 85 165 170 175  
 86 Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala  
 87 180 185 190  
 88 Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Ala Arg Ala Cys Gln  
 89 195 200 205  
 90 Asn Tyr Leu Lys Lys Thr  
 91 210

93 (2) INFORMATION FOR SEQ ID NO: 2:

95 (i) SEQUENCE CHARACTERISTICS:

96 (A) LENGTH: 2051 base pairs

97 (B) TYPE: nucleic acid

98 (C) STRANDEDNESS: single

99 (D) TOPOLOGY: linear

101 (vii) IMMEDIATE SOURCE:

102 (A) LIBRARY: MUSCNOT07

103 (B) CLONE: 3014759

105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

107 TCAGTTTCCT GCCAATGACG CTGGGGCAGC CGGGGCAGCC GGGGCAGCCC GGTCACCCCG 60  
 108 CCCCCAGGCC CACACTAAGG GTGTCCGCGG CCTGCCCTCC AGGCGGAGGA GCCCGGACTG 120  
 109 CGGAAGGATG GAGCTGGCCG CCGGAAGCTT CTCGGAGGAG CAGTTCTGGG AGGCCTGCGC 180  
 110 CGAGCTCCAG CAGCCCCTC TGGCCGGGGC GACTGGCAG CTCCTAGTGG AGACCTCGGG 240  
 111 CATCAGCATC TACCGGCTGC TGGACAAGAA GACTGGACTT TATGAGTATA AAGTCTTTGG 300  
 112 TGTTCTGGAG GACTGCTCAC CAACTCTACT GGCAGACATC TATATGGACT CAGATTACAG 360  
 113 AAAACAATGG GACCAGTATG TTAAAGAAGT CTATGAACAA GAATGCAACG GAGAGACTGT 420  
 114 GGTCTACTGG GAAGTGAAGT ACCCTTTTCC CATGTCCAAC AGAGACTATG TCTACCTTCG 480  
 115 GCAGCGGCGA GACCTGGACA TGGAAGGGAG GAAGATCCAT GTGATCCTGG CCCGGAGCAC 540  
 116 CTCCATGCCT CAGCTTGGCG AGAGGTCTGG GGTGATCCGG GTGAAGCAAT ACAAGCAGAG 600

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```

117 CCTGGCGATT GAGAGTGACG GCAAGAAGGG GAGCAAAGTT TTCATGTATT ACTTCGATAA 660
118 CCCGGGTGGC CAAATTCCGT CCTGGCTCAT TAACTGGGCC GCCAAGAATG GAGTTCCTAA 720
119 CTTCTTGAAA GACATGGCAA GAGCCTGTCA GAACTACCTC AAGAAAACCT AAGAAAAGAGA 780
120 ACTGGGAACA TTGCATCCAT GGGTTGATGT CTCTGGAAGT GCAACCACCC AATGTCTCTG 840
121 GAAGTGCCAC CTGGAAGTGC CACCTGGAAG TGTCTCTGGA AGAGCACCCA CCACTGTTCA 900
122 GCCTTCCCTT GCTGTTTCTG TCTTCAGAGG CCTACACACT ACCACATCCT TTCTAAGCAT 960
123 GTTTGCCTGA CATCCAGCTC ACTCGTCTGC TTCCTTTCTC GCTCCCCCCC ATCCTGGGGC 1020
124 TGGGGCTGCC TTCTTCTACA GTTCAATATG GGGCAGACTA GGGAAACCTT TGCTTGCTTA 1080
125 CTATTAGGAG GGAAGTCTT CAGTAGGGAA CACGATCATT CCATTGTGCA ATTTTACGGG 1140
126 GATGGGTGGG CGGAGGGACA CAACAAAATT TAAGAATGAC TATTTGGGCG GGCTGGCTCT 1200
127 TTTGCAGCTT GTGATTTCTT CCAGCTTGGG AGGGGCTGCT GGAAGTGGCA TTTCGTTTCA 1260
128 AGCTGACTTT CAGTGCACCC AAAGTGGATG ACGTGCCAAT GTCCATTTGC CTTATGCTTT 1320
129 GTGGAGCTGA TTAGGCTGGG ATTTGAGGTG ATAATCCAGT AAGTCTTTCC TCGTTCCTAC 1380
130 TTGTGGAGGA TCAGTAGCTG TTATGATGCC AGACCATTG GAGAAGTATC AGAGGCCTGA 1440
131 CCGGACACAT AATACGACAA CCACATTTTT CCTCATCATC CATGAGGAAA TGGATGATTT 1500
132 CTCTTTTCCA TATGTCACTG GGGGAAAGGC TGCCTGTACC TCTCAAGCTT TGCATTTTAC 1560
133 TGGAAACTGA GCGCTCAAGA TGGCTGTGGC CAGCTAGCAA AAGCAAAGAT GCTTTGTGCA 1620
134 TAGCCTTGTG AAAAAGTATC TTTCTATGCA ATAAGATGAA TTTTCCTCCC AGAATATTTA 1680
135 GAAATGTAGA AGGGATAACA GTTCACAGCC AGGTAAAATT TAACTGGTGG CTTAATGACT 1740
136 CTGCACCTTT TTCTCAGGAA TTCTGCCTAA GTTGTCTGCC TTTTCTACCA CCAAAAAGAC 1800
137 TTTTAGTTTT CTATGCTTTC TCCTGAATTT TGGTAGGGTA AGGTATTTCT ATGTCAAAGG 1860
138 CACAGCCTTG ATGATCTCAG GGAAAAATTT TAATCACTGT GTATAATGAT ACTGAACCTT 1920
139 GATTAATAAC AGAAATTCAG GATGTAAAGC CACAGAATGG GATTTATTAA TGTGGGATAC 1980
140 CTCAGACTGT TTGTTTTCTT TCTGGGAAGA AAAGTGTGTT CTATAATGAA TAAATATAGA 2040
141 GTGGTTTTTA A 2051

```

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGTUT12

(B) CLONE: 3126479

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

157 Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
158 1 5 10 15
159 Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
160 20 25 30
161 Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
162 35 40 45
163 Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
164 50 55 60
165 Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
166 65 70 75 80
167 Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
168 85 90 95
169 Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
170 100 105 110

```

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Input Set : N:\Crf3\RULE60\09879401.raw.txt

Output Set: N:\CRF4\01092003\I879401A.raw

```

171 Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Glu Gly Lys Ile
172      115      120      125
173 Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
174      130      135      140
175 Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
176      145      150      155      160
177 Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
178      165      170      175
179 Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
180      180      185      190
181 Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
182      195      200      205
184 Pro Arg Gly Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
185      210      215      220
186 Ala Ala Cys
187 225

```

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12
- (B) CLONE: 3126479

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

203 AGTACTTGTG TCCGGGTGGT GGACTGGATT CGCTGCGGAG CCCTGGAAGC TGCCTTTTCCT      60
204 TCTCCCTGTG CTTAACCAGA GGTGCCCATG GGTGGACAA TGAGGCTGGT CACAGCAGCA      120
205 CTGTTACTGG GTCTCATGAT GGTGGTCACT GGAGACGAGG ATGAGAACAG CCCGTGTGCC      180
206 CATGAGGCCC TCTTGACGA GGACACCCTC TTTTGCCAGG GCCTTGAAGT TTTCTACCCA      240
207 GAGTTGGGGA ACATTGGCTG CAAGGTTGTT CCTGATTGTA ACAACTACAG ACAGAAGATC      300
208 ACCTCCTGGA TGGAGCCGAT AGTCAAGTTC CCGGGGGCCG TGGACGGCGC AACCTATATC      360
209 CTGGTGATGG TGGATCCAGA TGCCCCTAGC AGAGCAGAAC CCAGACAGAG ATTCTGGAGA      420
210 CATTGGCTGG TAACAGATAT CAAGGGCGCC GACCTGAAGG AAGGGAAGAT TCAGGGCCAG      480
211 GAGTTATCAG CCTACCAGGC TCCCTCCCCA CCGGCACACA GTGGCTTCCA TCGCTACCAG      540
212 TTCTTTGTCT ATCTTCAGGA AGGAAAAGTC ATCTCTCTCC TTCCAAGGA AAACAAAAC      600
213 CGAGGCTCTT GGAAAATGGA CAGATTTCTG AACCGCTTCC ACCTGGGCGA ACCTGAAGCA      660
214 AGCACCCAGT TCATGACCCA GAACTACCAG GACTCACCAA CCCTCCAGGC TCCCAGAGGA      720
215 AGGGCCAGCG AGCCCAAGCA CAAAAACCAG GCGGAGATAG CTGCCTGCTA GATAGCCGGC      780
216 TTTGCCATCC GGGCATGTGG CCACACTGCC CACCACCGAC GATGTGGGTA TGGAACCCCC      840
217 TCTGGATACA GAACCCCTTC TTTTCCAAAT AAAAAAAAAA TCATCCAGGG CTTGGTGCTT      900
218 TGT

```

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,401A

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Input Set : N:\Crf3\RULE60\09879401.raw.txt

Output Set: N:\CRF4\01092003\I879401A.raw

229 (A) LIBRARY: GenBank  
 230 (B) CLONE: 897693  
 232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 234 Met Asp Pro Gly Ala Gly Ala Phe Ser Glu Glu Gln Phe Arg Glu Ala  
 235 1 5 10 15  
 236 Cys Ala Glu Leu Gln Arg Pro Ala Leu Ser Gly Ala Ala Trp Glu Leu  
 237 20 25 30  
 238 Leu Val Glu Thr Gln Gly Ile Ser Val Tyr Arg Leu Leu Asp Gln Gln  
 239 35 40 45  
 240 Thr Gly Leu Tyr Ala Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Leu  
 241 50 55 60  
 242 Pro Asp Leu Leu Ala Asp Val Tyr Met Asp Leu Ala Tyr Arg Lys Gln  
 243 65 70 75 80  
 245 Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Lys Glu Cys Ser Gly Glu  
 246 85 90 95  
 247 Thr Val Val Tyr Trp Gln Val Lys Tyr Pro Phe Pro Met Ser Asn Arg  
 248 100 105 110  
 249 Asp Tyr Val Tyr Val Arg Gln Arg Gln Glu Leu Asp Phe Glu Gly Gln  
 250 115 120 125  
 251 Lys Val His Val Ile Leu Ala Gln Ser Thr Ser Glu Pro Gln Phe Pro  
 252 130 135 140  
 253 Glu Lys Ser Gly Val Ile Arg Val Lys His Tyr Lys Gln Arg Leu Ala  
 254 145 150 155 160  
 255 Ile Gln Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe  
 256 165 170 175  
 257 Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Val Ile Asn Trp Ala Ala  
 258 180 185 190  
 259 Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Val Lys Ala Cys Gln  
 260 195 200 205  
 261 Asn Tyr Lys Lys Thr  
 262 210  
 264 (2) INFORMATION FOR SEQ ID NO: 6:  
 266 (i) SEQUENCE CHARACTERISTICS:  
 267 (A) LENGTH: 152 amino acids  
 268 (B) TYPE: amino acid  
 269 (C) STRANDEDNESS: single  
 270 (D) TOPOLOGY: linear  
 272 (vii) IMMEDIATE SOURCE:  
 273 (A) LIBRARY: GenBank  
 274 (B) CLONE: 1143527  
 276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 278 Val Val Ser Thr Ser Pro Thr Lys Leu Val Asn Val Ser Tyr Asn Asn  
 279 1 5 10 15  
 280 Leu Thr Val Asn Leu Gly Asn Glu Leu Thr Pro Thr Gln Val Lys Asn  
 281 20 25 30  
 282 Gln Pro Thr Lys Val Ser Trp Asp Ala Glu Pro Gly Ala Leu Tyr Thr  
 283 35 40 45  
 284 Leu Val Met Thr Asp Pro Asp Ala Pro Ser Arg Lys Asn Pro Val Phe  
 285 50 55 60

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/879,401A

DATE: 01/09/2003

TIME: 07:48:10

Input Set : N:\Crf3\RULE60\09879401.raw.txt

Output Set: N:\CRF4\01092003\I879401A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]